

CRF Errors Corrected by th STIC Systems Branch

O1PE

Serial Numb r: 09/874,198

CRF Processing Date:

Edited by:

Verified by:

3/11/2002

3

- Changed a file from non-ASCII to ASCII
- Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- Edited a format error in the Current Application Data section, specifically:
-
- Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____.
- Added the mandatory heading and subheadings for "Current Application Data".
- Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- Changed the spelling of a mandatory field (the headings or subheadings), specifically:
-
- Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
-
- Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
-
- Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- Inserted colons after headings/subheadings. Headings edited included:
-
- Deleted extra, invalid, headings used by an applicant, specifically:
-
- Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____.
- Inserted mandatory headings, specifically:
-
- Corrected an obvious error in the response, specifically:
-
- Edited identifiers where upper case is used but lower case is required, or vice versa.
- Corrected an error in the Number of Sequences field, specifically:
-
- A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- Other: Seq.1 - corrected amino acid numbering
-
-

* Examiner: Th abov corrections must b communicated to th applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING DATE: 03/11/2002
PATENT APPLICATION: US/09/874,198 **TIME:** 18:09:09

Input Set : N:\Crf3\02262002\I874198.raw
Output Set: N:\CRF3\03112002\I874198.raw

```

1 <110> APPLICANT: Jensenius, Jens Chr.
2     Thiel, Steffen
3 <120> TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND
4     USES FOR IT
5 <130> FILE REFERENCE: 09011-002002
6 <140> CURRENT APPLICATION NUMBER: US/09/874,198
7 <141> CURRENT FILING DATE: 2001-06-04
8 <150> PRIOR APPLICATION NUMBER: 09/054,218
9 <151> PRIOR FILING DATE: 1998-04-02
10 <150> PRIOR APPLICATION NUMBER: 60/042,678
11 <151> PRIOR FILING DATE: 1997-04-03
12 <160> NUMBER OF SEQ ID NOS: 8
13 <170> SOFTWARE: FastSEQ for Windows Version 4.0
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 41
17 <212> TYPE: PRT
18 <213> ORGANISM: Homo sapiens
19 <400> SEQUENCE: 1
20     Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala
21         1             5           10          15
22     Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
23         20            25           30
24     Thr Leu Thr Ala Pro Pro Gly Tyr Arg
25         35            40
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 686
29 <212> TYPE: PRT
30 <213> ORGANISM: Homo sapiens
31 <400> SEQUENCE: 2
32     Met Arg Leu Leu Thr Leu Leu Gly Leu Leu Cys Gly Ser Val Ala Thr
33         1             5           10          15
34     Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
35         20            25           30
36     Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
37         35            40           45
38     Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
39         50            55           60
40     Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
41         65            70           75          80
42     Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
43         85            90           95
44     Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
45         100           105          110

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46 Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
47 115 120 125
48 Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
49 130 135 140
50 Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
51 145 150 155 160
52 Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
53 165 170 175
54 Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
55 180 185 190
56 Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
57 195 200 205
58 Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
59 210 215 220
60 Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
61 225 230 235 240
62 Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
63 245 250 255
64 Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
65 260 265 270
66 Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
67 275 280 285
68 Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro Met
69 290 295 300
70 Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile Leu
71 305 310 315 320
72 Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu Gln
73 325 330 335
74 Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
75 340 345 350
76 Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly Pro
77 355 360 365
78 Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro Gly
79 370 375 380
80 Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
81 385 390 395 400
82 Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp Gly
83 405 410 415
84 Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu Pro
85 420 425 430
86 Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly Gly
87 435 440 445
88 Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu Gly
89 450 455 460
90 Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu Thr
91 465 470 475 480
92 Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu Asp
93 485 490 495
94 Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala

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95	500	505	510
96	Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala Gly		
97	515	520	525
98	Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val Ile		
99	530	535	540
100	Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu Ser		
101	545	550	555
102	Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu Thr		
103	565	570	575
104	Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro Ile		
105	580	585	590
106	Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr Pro		
107	595	600	605
108	Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly		
109	610	615	620
110	Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu		
111	625	630	635
112	Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly		
113	645	650	655
114	Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val		
115	660	665	670
116	Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser Asp Phe		
117	675	680	685
119	<210> SEQ ID NO: 3		
120	<211> LENGTH: 2475		
121	<212> TYPE: DNA		
122	<213> ORGANISM: Homo sapiens		
123	<220> FEATURE:		
124	<221> NAME/KEY: CDS		
125	<222> LOCATION: (37)...(2094)		
126	<400> SEQUENCE: 3		
127	ctcgtgcaat tcggcacgag gctggacggg cacacc atg agg ctg ctg acc ctc		54
128	Met Arg Leu Leu Thr Leu		
129	1 5		
130	ctg ggc ctt ctg tgt ggc tcg gtg gcc acc ccc tta ggc ccg aag tgg		102
131	Leu Gly Leu Leu Cys Gly Ser Val Ala Thr Pro Leu Gly Pro Lys Trp		
132	10 15 20		
133	cct gaa cct gtg ttc ggg cgc ctg gca tcc ccc ggc ttt cca ggg gag		150
134	Pro Glu Pro Val Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu		
135	25 30 35		
136	tat gcc aat gac cag gag cgg cgc tgg acc ctg act gca ccc ccc ggc		198
137	Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr Leu Thr Ala Pro Pro Gly		
138	40 45 50		
139	tac cgc ctg cgc ctc tac ttc acc cac ttc gac ctg gag ctc tcc cac		246
140	Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser His		
141	55 60 65 70		
142	ctc tgc gag tac gac ttc gtc aag ctg agc tcg ggg gcc aag gtg ctg		294
143	Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser Ser Gly Ala Lys Val Leu		
144	75 80 85		

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145	gcc acg ctg tgc ggg cag gag agc aca gac acg gag cg	342
146	Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly	
147	90 95 100	
148	aag gac act ttc tac tcg ctg ggc tcc agc ctg gac att acc ttc cgc	390
149	Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg	
150	105 110 115	
151	tcc gac tac tcc aac gag aag ccg ttc acg ggg ttc gag gcc ttc tat	438
152	Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr	
153	120 125 130	
154	gca gcc gag gac att gac gag tgc cag gtg gcc ccg gga gag gcg ccc	486
155	Ala Ala Glu Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro	
156	135 140 145 150	
157	acc tgc gac cac cac tgc cac aac cac ctg ggc ggt ttc tac tgc tcc	534
158	Thr Cys Asp His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser	
159	155 160 165	
160	tgc cgc gca ggc tac gtc ctg cac cgt aac aag ccg acc tgc tca gcc	582
161	Cys Arg Ala Gly Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Ala	
162	170 175 180	
163	ctg tgc tcc ggc cag gtc ttc acc cag agg tct ggg gag ctc agc agc	630
164	Leu Cys Ser Gly Gln Val Phe Thr Gln Arg Ser Gly Glu Leu Ser Ser	
165	185 190 195	
166	cct gaa tac cca cgg ccg tat ccc aaa ctc tcc agt tgc act tac agc	678
167	Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu Ser Ser Cys Thr Tyr Ser	
168	200 205 210	
169	atc agc ctg gag ggg ttc agt gtc att ctg gac ttt gtg gag tcc	726
170	Ile Ser Leu Glu Glu Phe Ser Val Ile Leu Asp Phe Val Glu Ser	
171	215 220 225 230	
172	ttc gat gtg gag aca cac cct gaa acc ctg tgt ccc tac gac ttt ctc	774
173	Phe Asp Val Glu Thr His Pro Glu Thr Leu Cys Pro Tyr Asp Phe Leu	
174	235 240 245	
175	aag att caa aca gac aga gaa gaa cat ggc cca ttc tgt ggg aag aca	822
176	Lys Ile Gln Thr Asp Arg Glu Glu His Gly Pro Phe Cys Gly Lys Thr	
177	250 255 260	
178	ttg ccc cac agg att gaa aca aaa agc aac acg gtg acc atc acc ttt	870
179	Leu Pro His Arg Ile Glu Thr Lys Ser Asn Thr Val Thr Ile Thr Phe	
180	265 270 275	
181	gtc aca gat gaa tca gga gac cac aca ggc tgg aag atc cac tac acg	918
182	Val Thr Asp Glu Ser Gly Asp His Thr Gly Trp Lys Ile His Tyr Thr	
183	280 285 290	
184	agc aca gcg cag cct tgc cct tat ccg atg gcg cca cct aat ggc cac	966
185	Ser Thr Ala Gln Pro Cys Pro Tyr Pro Met Ala Pro Pro Asn Gly His	
186	295 300 305 310	
187	gtt tca cct gtgcaa gcc aaa tac atc ctg aaa gac agc ttc tcc atc	1014
188	Val Ser Pro Val Gln Ala Lys Tyr Ile Leu Lys Asp Ser Phe Ser Ile	
189	315 320 325	
190	ttt tgc gag act ggc tat gag ctt ctg caa ggt cac ttg ccc ctg aaa	1062
191	Phe Cys Glu Thr Gly Tyr Glu Leu Leu Gln Gly His Leu Pro Leu Lys	
192	330 335 340	
193	tcc ttt act gca gtt tgt cag aaa gat gga tct tgg gac cgg cca atg	1110

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194	Ser Phe Thr Ala Val Cys Gln Lys Asp Gly Ser Trp Asp Arg Pro Met			
195	345	350	355	
196	ccc gcg tgc agc att gtt gac tgt ggc cct cct gat gat cta ccc agt		1158	
197	Pro Ala Cys Ser Ile Val Asp Cys Gly Pro Pro Asp Asp Leu Pro Ser			
198	360	365	370	
199	ggc cga gtg gag tac atc aca ggt cct gga gtg acc acc tac aaa gct		1206	
200	Gly Arg Val Glu Tyr Ile Thr Gly Pro Gly Val Thr Thr Tyr Lys Ala			
201	375	380	385	390
202	gtg att cag tac agc tgt gaa gag acc ttc tac aca atg aaa gtg aat		1254	
203	Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe Tyr Thr Met Lys Val Asn			
204	395	400	405	
205	gat ggt aaa tat gtg tgt gag gct gat gga ttc tgg acg agc tcc aaa		1302	
206	Asp Gly Lys Tyr Val Cys Glu Ala Asp Gly Phe Trp Thr Ser Ser Lys			
207	410	415	420	
208	gga gaa aaa tca ctc cca gtc tgt gag cct gtt tgt gga cta tca gcc		1350	
209	Gly Glu Lys Ser Leu Pro Val Cys Glu Pro Val Cys Gly Leu Ser Ala			
210	425	430	435	
211	cgc aca aca gga ggg cgt ata tat gga ggg caa aag gca aaa cct ggt		1398	
212	Arg Thr Thr Gly Arg Ile Tyr Gly Gly Gln Lys Ala Lys Pro Gly			
213	440	445	450	
214	gat ttt cct tgg caa gtc ctg ata tta ggt gga acc aca gca gca ggt		1446	
215	Asp Phe Pro Trp Gln Val Leu Ile Leu Gly Gly Thr Thr Ala Ala Gly			
216	455	460	465	470
217	gca ctt tta tat gac aac tgg gtc cta aca gct gct cat gcc gtc tat		1494	
218	Ala Leu Leu Tyr Asp Asn Trp Val Leu Thr Ala Ala His Ala Val Tyr			
219	475	480	485	
220	gag caa aaa cat gat gca tcc gcc ctg gac att cga atg ggc acc ctg		1542	
221	Glu Gln Lys His Asp Ala Ser Ala Leu Asp Ile Arg Met Gly Thr Leu			
222	490	495	500	
223	aaa aga cta tca cct cat tat aca caa gcc tgg tct gaa gct gtt ttt		1590	
224	Lys Arg Leu Ser Pro His Tyr Thr Gln Ala Trp Ser Glu Ala Val Phe			
225	505	510	515	
226	ata cat gaa ggt tat act cat gat gct ggc ttt gac aat gac ata gca		1638	
227	Ile His Glu Gly Tyr Thr His Asp Ala Gly Phe Asp Asn Asp Ile Ala			
228	520	525	530	
229	ctg att aaa ttg aat aac aaa gtt gta atc aat agc aac atc acg cct		1686	
230	Leu Ile Lys Leu Asn Asn Lys Val Val Ile Asn Ser Asn Ile Thr Pro			
231	535	540	545	550
232	att tgt ctg cca aga aaa gaa gct gaa tcc ttt atg agg aca gat gac		1734	
233	Ile Cys Leu Pro Arg Lys Glu Ala Glu Ser Phe Met Arg Thr Asp Asp			
234	555	560	565	
235	att gga act gca tct gga tgg gga tta acc caa agg ggt ttt ctt gct		1782	
236	Ile Gly Thr Ala Ser Gly Trp Gly Leu Thr Gln Arg Gly Phe Leu Ala			
237	570	575	580	
238	aga aat cta atg tat gtc gac ata ccg att gtt gac cat caa aaa tgt		1830	
239	Arg Asn Leu Met Tyr Val Asp Ile Pro Ile Val Asp His Gln Lys Cys			
240	585	590	595	
241	act gct gca tat gaa aag cca ccc tat cca agg gga agt gta act gct		1878	
242	Thr Ala Ala Tyr Glu Lys Pro Pro Tyr Pro Arg Gly Ser Val Thr Ala			

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